

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/577,613A
Source: FWO
Date Processed by STIC: 2/21/06

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/577,613A

CRF Edit Date: 12/21/06
Edited by: h

___ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

___ Corrected the SEQ ID NO. Sequence numbers edited were:

___ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

___ Deleted: ___ invalid beginning/end-of-file text ; ___ page numbers

___ Inserted mandatory headings/numeric identifiers, specifically:

___ Moved responses to same line as heading/numeric identifier, specifically:

✓
___ Other: moved prior application number from insertion
title line to prior application data section



IFWO

RAW SEQUENCE LISTING

DATE: 12/21/2006

PATENT APPLICATION: US/10/577,613A

TIME: 10:27:51

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\12212006\J577613A.raw

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3 <110> APPLICANT: Cherkasky, Alexander
5 <120> TITLE OF INVENTION: CHERKASKY PROTEINS CONTAINING ANTIBODY-,
6     ANTIGEN- AND MICROTUBULE-BINDING REGIONS AND IMMUNE
7     RESPONSE-TRIGGERING REGIONS
9 <130> FILE REFERENCE: -
11 <140> CURRENT APPLICATION NUMBER: US/10/577,613A
C--> 12 <141> CURRENT FILING DATE: 2006-04-28
14 <150> PRIOR APPLICATION NUMBER: PCT/IB 2004/003536
15 <151> PRIOR FILING DATE: 2004-10-28
17 <160> NUMBER OF SEQ ID NOS: 14
19 <170> SOFTWARE: PatentIn version 3.4
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 676
23 <212> TYPE: PRT
24 <213> ORGANISM: Artificial
26 <220> FEATURE:
27 <223> OTHER INFORMATION: 1a SPA-5G-gephyrin
30 <220> FEATURE:
W--> 31 <221> NAME/KEY: FUSION PRT
32 <222> LOCATION: (1)..(676)
33 <223> OTHER INFORMATION: fusion protein Staph. aureus Protein A and H. sapiens
gephyrin
35 <400> SEQUENCE: 1
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38 1             5             10             15
41 Asn Met Pro Asn Leu Asn Ala Asp Gln Arg Asn Gly Phe Ile Gln Ser
42             20             25             30
45 Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Val Leu Gly Glu Ala Lys
46             35             40             45
49 Lys Leu Asn Glu Ser Gln Ala Pro Lys Ala Asp Asn Asn Phe Asn Lys
50             50             55             60
53 Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu Asn Met Pro Asn Leu Asn
54 65             70             75             80
57 Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser
58             85             90             95
61 Gln Ser Ala Asn Leu Leu Ser Glu Ala Lys Lys Leu Asn Glu Ser Gln
62             100            105            110
65 Ala Pro Lys Ala Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe
66             115            120            125
69 Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Gly
70             130            135            140
73 Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu
74 145            150            155            160
77 Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Asp Asn

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78          165          170          175
81 Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu
82          180          185          190
85 Pro Asn Leu Thr Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys
86          195          200          205
89 Asp Asp Pro Ser Val Ser Lys Glu Ile Leu Ala Glu Ala Lys Lys Leu
90          210          215          220
93 Asn Asp Ala Gln Ala Pro Lys Glu Glu Asp Asn Asn Lys Pro Gly Lys
94 225          230          235          240
97 Glu Asp Gly Asn Lys Pro Gly Lys Glu Asp Gly Asn Gly Gly Gly Gly
98          245          250          255
101 Gly Met Ser Pro Phe Pro Leu Thr Ser Met Asp Lys Ala Phe Ile Thr
102          260          265          270
105 Val Leu Glu Met Thr Pro Val Leu Gly Thr Glu Ile Ile Asn Tyr Arg
106          275          280          285
109 Asp Gly Met Gly Arg Val Leu Ala Gln Asp Val Tyr Ala Lys Asp Asn
110          290          295          300
113 Leu Pro Pro Phe Pro Ala Ser Val Lys Asp Gly Tyr Ala Val Arg Ala
114 305          310          315          320
117 Ala Asp Gly Pro Gly Asp Arg Phe Ile Ile Gly Glu Ser Gln Ala Gly
118          325          330          335
121 Glu Gln Pro Thr Gln Thr Val Met Pro Gly Gln Val Met Arg Val Thr
122          340          345          350
125 Thr Gly Ala Pro Ile Pro Cys Gly Ala Asp Ala Val Val Gln Val Glu
126          355          360          365
129 Asp Thr Glu Leu Ile Arg Glu Ser Asp Asp Gly Thr Glu Glu Leu Glu
130          370          375          380
133 Val Arg Ile Leu Val Gln Ala Arg Pro Gly Gln Asp Ile Arg Pro Ile
134 385          390          395          400
137 Gly His Asp Ile Lys Arg Gly Glu Cys Val Leu Ala Lys Gly Thr His
138          405          410          415
141 Met Gly Pro Ser Glu Ile Gly Leu Leu Ala Thr Val Gly Val Thr Glu
142          420          425          430
145 Val Glu Val Asn Lys Phe Pro Val Val Ala Val Met Ser Thr Gly Asn
146          435          440          445
149 Glu Leu Leu Asn Pro Glu Asp Asp Leu Leu Pro Gly Lys Ile Arg Asp
150          450          455          460
153 Ser Asn Arg Ser Thr Leu Leu Ala Thr Ile Gln Glu His Gly Tyr Pro
154 465          470          475          480
157 Thr Ile Asn Leu Gly Ile Val Gly Asp Asn Pro Asp Asp Leu Leu Asn
158          485          490          495
161 Ala Leu Asn Glu Gly Ile Ser Arg Ala Asp Val Ile Ile Thr Ser Gly
162          500          505          510
165 Gly Val Ser Met Gly Glu Lys Asp Tyr Leu Lys Gln Val Leu Asp Ile
166          515          520          525
169 Asp Leu His Ala Gln Ile His Phe Gly Arg Val Phe Met Lys Pro Gly
170          530          535          540
173 Leu Pro Thr Thr Phe Ala Thr Leu Asp Ile Asp Gly Val Arg Lys Ile
174 545          550          555          560

```

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177 Ile Phe Ala Leu Pro Gly Asn Pro Val Ser Ala Val Val Thr Cys Asn
178           565           570           575
181 Leu Phe Val Val Pro Ala Leu Arg Lys Met Gln Gly Ile Leu Asp Pro
182           580           585           590
185 Arg Pro Thr Ile Ile Lys Ala Arg Leu Ser Cys Asp Val Lys Leu Asp
186           595           600           605
189 Pro Arg Pro Glu Tyr His Arg Cys Ile Leu Thr Trp His His Gln Glu
190           610           615           620
193 Pro Leu Pro Trp Ala Gln Ser Thr Gly Asn Gln Met Ser Ser Arg Leu
194 625           630           635           640
197 Met Ser Met Arg Ser Ala Asn Gly Leu Leu Met Leu Pro Pro Lys Thr
198           645           650           655
201 Glu Gln Tyr Val Glu Leu His Lys Gly Glu Val Val Asp Val Met Val
202           660           665           670
205 Ile Gly Arg Leu
206           675

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209 <210> SEQ ID NO: 2

210 <211> LENGTH: 2092

211 <212> TYPE: DNA

212 <213> ORGANISM: Artificial

214 <220> FEATURE:

215 <223> OTHER INFORMATION: 1b SPA-5G-gephyrin

218 <220> FEATURE:

219 <221> NAME/KEY: misc_recomb

220 <222> LOCATION: (1)..(2092)

221 <223> OTHER INFORMATION: nucleic acid encoding Staph. aureus Protein A and H. sapiens
 222 gephyrin fusion prt

224 <400> SEQUENCE: 2

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225 tgctgcgcaa cagcatgaag ctcaacaaaa cgcttttttat caagtcttaa atatgcctaa      60
227 cttaaatgct gatcaacgca atgggttttat ccaaagcctt aaagatgata caagccaaag      120
229 tgctaacggt ttaggtgaag ctaaaaaatt aaacgaatct caagcaccga aagctgacaa      180
231 caatttcaac aaagaacaac aaaatgcttt ctatgaaatc ttgaacatgc ctaacttgaa      240
233 cgaagaacaa cgcaatgggt tcatccaaag cttaaaagat gacccaagtc aaagtgttaa      300
235 cctattgtca gaagctaaaa agttaaatga atctcaagca ccgaaagcgg ataacaaatt      360
237 caacaaagaa caacaaaatg ctttctatga aatcttacat ttacctaaact taaacgaaga      420
239 acaacgcaat ggtttcatcc aaagcctaaa agatgaccca agccaaagcg ctaacctttt      480
241 agcagaagct aaaaagctaa atgatgcaca agcaccacaaa gctgacaaca aattcaacaa      540
243 agaacaacaa aatgctttct atgaaatttt acatttacct aacttaactg aagagcaacg      600
245 taacggcttc atccaaagcc ttaaagacga tccttcagtg agcaaagaaa ttttagcaga      660
247 agctaaaaag ctaaacgatg ctcaagcacc aaaagaggaa gacaacaaca aacctggtaa      720
249 agaagacggc acaaacctg gcaaagaaga cggtaacggc ggcggcggcg gcgtttagggt      780
251 cacagtgtcg tcgatatac caaggtgggt agaagacatc gcatgtctcc ttttcctctg      840
253 acatctatgg acaaagcctt tatcacagtc ctggagatga ctccggtgct tgggacagaa      900
255 atcatcaatt accgagatgg aatggggcga gtccttgctc aagatgtata tgcaaaagac      960
257 aatttacccc ctttcccagc atcagtaaaa gatggctatg ctgtccgagc tgctgatggc      1020
259 ccaggagatc gtttcatcat tggggaatcc caagctggtg aacagccaac tcagacagta      1080
261 atgccaggac aagtcatgcy gggtacaaca ggtgctccaa taccctgcgg tgctgatgca      1140
263 gtagtacaag tggaagatac cgaacttatc agggaatcag atgatggcac tgaagaactt      1200
265 gaagtgcgaa ttctggtgca agctcggcca ggccaagata tcagacccat cggccatgac      1260

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Input Set : A:\PTO.AMC.txt

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267 attaaaagag ggggaatgtgt tttggccaaa ggaacccaca tgggcccctc agagattggt 1320
269 cttctggcaa ctgtagggtgt cacagagggt gaagttaata agtttccagt ggttgcagtc 1380
271 atgtcaacag ggaatgagct gctaaatcct gaagatgacc tcttaccagg gaagattcga 1440
273 gacagcaatc gttcaactct tctagcaaca attcaggaac atggttaccc cacgatcaac 1500
275 ttgggtattg taggagacaa cccagatgac ttactcaatg ccttgaatga gggatatcagt 1560
277 cgtgctgatg tcatcatcac atcaggggggt gtatccatgg gggaaaagga ctatctcaag 1620
279 caggtgctgg acattgatct tcatgctcag atccattttg gcaggggttt tatgaaacca 1680
281 ggcttgccaa caacatttgc aactttggat attgatgggtg taagaaaaat aatctttgca 1740
283 ctacctggga atcctgtatc ggctgtgggtc acctgcaatc tctttgttgt gcctgcactg 1800
285 aggaaaatgc agggcatcct ggatcctcgg ccaaccatca tcaaagcaag gttatcatgt 1860
287 gatgtaaaac ttgatcctcg tccagaatac catcggtgta tactaacttg gcatcaccaa 1920
289 gaaccactac cttgggcaca gagtacaggt aatcaaatga gcagccgtct gatgagcatg 1980
291 cgcagtgcc atggattgtt gatgctacct ccaaagacag aacagtacgt ggagctccac 2040
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296 <210> SEQ ID NO: 3

297 <211> LENGTH: 300

298 <212> TYPE: PRT

299 <213> ORGANISM: Artificial

301 <220> FEATURE:

302 <223> OTHER INFORMATION: 2a SPA-5G-MBP

305 <220> FEATURE:

W--> 306 <221> NAME/KEY: FUSION_PRT

307 <222> LOCATION: (1)..(300)

308 <223> OTHER INFORMATION: Fusion Protein of Staph. aureus Protein A and H. sapiens MBP

310 <220> FEATURE:

311 <221> NAME/KEY: MISC_FEATURE

312 <222> LOCATION: (264)..(264)

313 <223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

315 <220> FEATURE:

316 <221> NAME/KEY: MISC_FEATURE

317 <222> LOCATION: (278)..(278)

318 <223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

320 <220> FEATURE:

321 <221> NAME/KEY: MISC_FEATURE

322 <222> LOCATION: (281)..(281)

323 <223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

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327 Ala Ala Gln His Asp Glu Ala Gln Gln Asn Ala Phe Tyr Gln Val Leu

328 1 5 10 15

331 Asn Met Pro Asn Leu Asn Ala Asp Gln Arg Asn Gly Phe Ile Gln Ser

332 20 25 30

335 Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Val Leu Gly Glu Ala Lys

336 35 40 45

339 Lys Leu Asn Glu Ser Gln Ala Pro Lys Ala Asp Asn Asn Phe Asn Lys

340 50 55 60

343 Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu Asn Met Pro Asn Leu Asn

344 65 70 75 80

347 Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser

348 85 90 95

RAW SEQUENCE LISTING

DATE: 12/21/2006

PATENT APPLICATION: US/10/577,613A

TIME: 10:27:51

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\12212006\J577613A.raw

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351 Gln Ser Ala Asn Leu Leu Ser Glu Ala Lys Lys Leu Asn Glu Ser Gln
352          100          105          110
355 Ala Pro Lys Ala Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe
356          115          120          125
359 Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Gly
360          130          135          140
363 Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu
364 145          150          155          160
367 Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Asp Asn
368          165          170          175
371 Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu
372          180          185          190
375 Pro Asn Leu Thr Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys
376          195          200          205
379 Asp Asp Pro Ser Val Ser Lys Glu Ile Leu Ala Glu Ala Lys Lys Leu
380          210          215          220
383 Asn Asp Ala Gln Ala Pro Lys Glu Glu Asp Asn Asn Lys Pro Gly Lys
384 225          230          235          240
387 Glu Asp Gly Asn Lys Pro Gly Lys Glu Asp Gly Asn Gly Gly Gly Gly
388          245          250          255
W--> 391 Gly Ala Ala Ala Ser Thr Ala Xaa Ala Ser Thr Ala Lys Glu Thr Ala
392          260          265          270
395 Glu Ala Val Ala Asp Xaa Ile Leu Xaa Lys Ala Gly Pro Leu Val Ala
396          275          280          285
399 Val Ser Ala Val Ala Leu Asp Ile Thr Ala Tyr Pro
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403 <210> SEQ ID NO: 4
404 <211> LENGTH: 912
405 <212> TYPE: DNA
406 <213> ORGANISM: Artificial
408 <220> FEATURE:
409 <223> OTHER INFORMATION: 2b SPA-5g-MBP
412 <220> FEATURE:
413 <221> NAME/KEY: misc_recomb
414 <222> LOCATION: (1)..(912)
415 <223> OTHER INFORMATION: nucleic acid encoding Staph. aureus Protein A and H. sapiens
MBP
416          fusion prt
418 <220> FEATURE:
419 <221> NAME/KEY: misc_feature
420 <222> LOCATION: (792)..(792)
421 <223> OTHER INFORMATION: n is a, c, g, t or u
423 <220> FEATURE:
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426 <223> OTHER INFORMATION: n is a, c, g, t or u
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429 <221> NAME/KEY: misc_feature
430 <222> LOCATION: (844)..(844)
431 <223> OTHER INFORMATION: n is a, c, g, t or u

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/577,613A

DATE: 12/21/2006
TIME: 10:27:52

FYI

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\12212006\J577613A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; Xaa Pos. 264,278,281
Seq#:4; N Pos. 792,835,844
Seq#:8; N Pos. 488,531,540
Seq#:9; N Pos. 440,483,492
Seq#:12; N Pos. 792,835,844

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8,9,10,11,12,13,14

VERIFICATION SUMMARY

DATE: 12/21/2006

PATENT APPLICATION: US/10/577,613A

TIME: 10:27:52

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\12212006\J577613A.raw

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:31 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:306 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:391 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:256
M:341 Repeated in SeqNo=3
L:460 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:780
M:341 Repeated in SeqNo=4
L:859 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:480
L:935 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:420
M:341 Repeated in SeqNo=9
L:1317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:780
M:341 Repeated in SeqNo=12

**Raw Sequence Listing before editing
(for reference only)**



IFWO

RAW SEQUENCE LISTING

DATE: 12/19/2006

PATENT APPLICATION: US/10/577,613A

TIME: 10:53:57

Input Set : A:\csequence listing.txt

Output Set: N:\CRF4\12192006\J577613A.raw

3 <110> APPLICANT: Cherkasky, Alexander
 5 <120> TITLE OF INVENTION: PCT/IB 2004/003536 CHERKASKY PROTEINS CONTAINING ANTIBODY-,
 6 ANTIGEN- AND MICROTUBULE-BINDING REGIONS AND IMMUNE
 7 RESPONSE-TRIGGERING REGIONS
 9 <130> FILE REFERENCE: -
 11 <140> CURRENT APPLICATION NUMBER: US/10/577,613A
 C--> 12 <141> CURRENT FILING DATE: 2006-04-28
 14 <160> NUMBER OF SEQ ID NOS: 14
 16 <170> SOFTWARE: PatentIn version 3.4
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 676
 20 <212> TYPE: PRT
 21 <213> ORGANISM: Artificial
 23 <220> FEATURE:
 24 <223> OTHER INFORMATION: 1a SPA-5G-gephyrin
 27 <220> FEATURE:
 W--> 28 <221> NAME/KEY: FUSION_PRT
 29 <222> LOCATION: (1)..(676)
 30 <223> OTHER INFORMATION: fusion protein Staph. aureus Protein A and H. sapiens
 gephyrin
 32 <400> SEQUENCE: 1
 34 Ala Ala Gln His Asp Glu Ala Gln Gln Asn Ala Phe Tyr Gln Val Leu
 35 1 5 10 15
 38 Asn Met Pro Asn Leu Asn Ala Asp Gln Arg Asn Gly Phe Ile Gln Ser
 39 20 25 30
 42 Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Val Leu Gly Glu Ala Lys
 43 35 40 45
 46 Lys Leu Asn Glu Ser Gln Ala Pro Lys Ala Asp Asn Asn Phe Asn Lys
 47 50 55 60
 50 Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu Asn Met Pro Asn Leu Asn
 51 65 70 75 80
 54 Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser
 55 85 90 95
 58 Gln Ser Ala Asn Leu Leu Ser Glu Ala Lys Lys Leu Asn Glu Ser Gln
 59 100 105 110
 62 Ala Pro Lys Ala Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe
 63 115 120 125
 66 Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Gly
 67 130 135 140
 70 Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu
 71 145 150 155 160
 74 Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Asp Asn
 75 165 170 175
 78 Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu

do NOT insert prior application data
 on invention title line
 1507 PCT/IB04/03536
 1517 2004-10-28
 Does Not Comply
 Corrected Diskette Needed

RAW SEQUENCE LISTING

DATE: 12/19/2006

PATENT APPLICATION: US/10/577,613A

TIME: 10:53:57

Input Set : A:\csequence listing.txt

Output Set: N:\CRF4\12192006\J577613A.raw

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79          180          185          190
82 Pro Asn Leu Thr Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys
83          195          200          205
86 Asp Asp Pro Ser Val Ser Lys Glu Ile Leu Ala Glu Ala Lys Lys Leu
87          210          215          220
90 Asn Asp Ala Gln Ala Pro Lys Glu Glu Asp Asn Asn Lys Pro Gly Lys
91 225          230          235          240
94 Glu Asp Gly Asn Lys Pro Gly Lys Glu Asp Gly Asn Gly Gly Gly Gly
95          245          250          255
98 Gly Met Ser Pro Phe Pro Leu Thr Ser Met Asp Lys Ala Phe Ile Thr
99          260          265          270
102 Val Leu Glu Met Thr Pro Val Leu Gly Thr Glu Ile Ile Asn Tyr Arg
103          275          280          285
106 Asp Gly Met Gly Arg Val Leu Ala Gln Asp Val Tyr Ala Lys Asp Asn
107          290          295          300
110 Leu Pro Pro Phe Pro Ala Ser Val Lys Asp Gly Tyr Ala Val Arg Ala
111 305          310          315          320
114 Ala Asp Gly Pro Gly Asp Arg Phe Ile Ile Gly Glu Ser Gln Ala Gly
115          325          330          335
118 Glu Gln Pro Thr Gln Thr Val Met Pro Gly Gln Val Met Arg Val Thr
119          340          345          350
122 Thr Gly Ala Pro Ile Pro Cys Gly Ala Asp Ala Val Val Gln Val Glu
123          355          360          365
126 Asp Thr Glu Leu Ile Arg Glu Ser Asp Asp Gly Thr Glu Glu Leu Glu
127          370          375          380
130 Val Arg Ile Leu Val Gln Ala Arg Pro Gly Gln Asp Ile Arg Pro Ile
131 385          390          395          400
134 Gly His Asp Ile Lys Arg Gly Glu Cys Val Leu Ala Lys Gly Thr His
135          405          410          415
138 Met Gly Pro Ser Glu Ile Gly Leu Leu Ala Thr Val Gly Val Thr Glu
139          420          425          430
142 Val Glu Val Asn Lys Phe Pro Val Val Ala Val Met Ser Thr Gly Asn
143          435          440          445
146 Glu Leu Leu Asn Pro Glu Asp Asp Leu Leu Pro Gly Lys Ile Arg Asp
147          450          455          460
150 Ser Asn Arg Ser Thr Leu Leu Ala Thr Ile Gln Glu His Gly Tyr Pro
151 465          470          475          480
154 Thr Ile Asn Leu Gly Ile Val Gly Asp Asn Pro Asp Asp Leu Leu Asn
155          485          490          495
158 Ala Leu Asn Glu Gly Ile Ser Arg Ala Asp Val Ile Ile Thr Ser Gly
159          500          505          510
162 Gly Val Ser Met Gly Glu Lys Asp Tyr Leu Lys Gln Val Leu Asp Ile
163          515          520          525
166 Asp Leu His Ala Gln Ile His Phe Gly Arg Val Phe Met Lys Pro Gly
167          530          535          540
170 Leu Pro Thr Thr Phe Ala Thr Leu Asp Ile Asp Gly Val Arg Lys Ile
171 545          550          555          560
174 Ile Phe Ala Leu Pro Gly Asn Pro Val Ser Ala Val Val Thr Cys Asn
175          565          570          575

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Input Set : A:\csequence listing.txt

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178 Leu Phe Val Val Pro Ala Leu Arg Lys Met Gln Gly Ile Leu Asp Pro
179          580          585          590
182 Arg Pro Thr Ile Ile Lys Ala Arg Leu Ser Cys Asp Val Lys Leu Asp
183          595          600          605
186 Pro Arg Pro Glu Tyr His Arg Cys Ile Leu Thr Trp His His Gln Glu
187          610          615          620
190 Pro Leu Pro Trp Ala Gln Ser Thr Gly Asn Gln Met Ser Ser Arg Leu
191 625          630          635          640
194 Met Ser Met Arg Ser Ala Asn Gly Leu Leu Met Leu Pro Pro Lys Thr
195          645          650          655
198 Glu Gln Tyr Val Glu Leu His Lys Gly Glu Val Val Asp Val Met Val
199          660          665          670
202 Ile Gly Arg Leu
203          675

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206 <210> SEQ ID NO: 2

207 <211> LENGTH: 2092

208 <212> TYPE: DNA

209 <213> ORGANISM: Artificial

211 <220> FEATURE:

212 <223> OTHER INFORMATION: 1b SPA-5G-gephyrin

215 <220> FEATURE:

216 <221> NAME/KEY: misc_recomb

217 <222> LOCATION: (1)..(2092)

218 <223> OTHER INFORMATION: nucleic acid encoding Staph. aureus Protein A and H. sapiens

219 gephyrin fusion prt

221 <400> SEQUENCE: 2

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222 tgctgcgcaa cagcatgaag ctcaacaaaa cgcttttttat caagtcttaa atatgcctaa      60
224 cttaaatgct gatcaacgca atgggttttat ccaaagcctt aaagatgatc caagccaaag      120
226 tgctaacggt ttaggtgaag ctaaaaaatt aaacgaatct caagcaccga aagctgacaa      180
228 caatttcaac aaagaacaac aaaatgcttt ctatgaaatc ttgaacatgc ctaacttgaa      240
230 cgaagaacaa cgcaatgggt tcattccaaag cttaaaagat gacccaagtc aaagtgctaa      300
232 cctattgtca gaagctaaaa agttaaatga atctcaagca ccgaaagcgg ataacaaatt      360
234 caacaaagaa caacaaaatg ctttctatga aatcttacat ttacctaaact taaacgaaga      420
236 acaacgcaat ggtttcatcc aaagcctaaa agatgaccca agccaaagcg ctaacctttt      480
238 agcagaagct aaaaagctaa atgatgcaca agcaccaaaa gctgacaaca aattcaacaa      540
240 agaacaacaa aatgctttct atgaaatttt acatttacct aacttaactg aagagcaacg      600
242 taacggcttc atccaaagcc ttaaagacga tccttcagtg agcaaagaaa ttttagcaga      660
244 agctaaaaag ctaaacgatg ctcaagcacc aaaagaggaa gacaacaaca aacctggtaa      720
246 agaagacggc acaaaacctg gcaaagaaga cggtaacggc ggcggcggcg gcgtttaggt      780
248 cacagtgtcg tcgatatcac caaggtggct agaagacatc gcatgtctcc ttttctctg      840
250 acatctatgg acaaagcctt tatcacagtc ctggagatga ctccggtgct tgggacagaa      900
252 atcatcaatt accgagatgg aatggggcga gtccttgctc aagatgtata tgcaaaagac      960
254 aatttacccc ctttcccagc atcagtaaaa gatggctatg ctgtccgagc tgctgatggc     1020
256 ccaggagatc gtttcatcat tggggaatcc caagctggtg aacagccaac tcagacagta     1080
258 atgccaggac aagtcatgcg gggtacaaca ggtgctccaa taccctgcgg tgctgatgca     1140
260 gtagtacaag tggaagatac cgaacttatc agggaatcag atgatggcac tgaagaactt     1200
262 gaagtgcgaa ttctgggtgca agctcggcca ggccaagata tcagacccat cggccatgac     1260
264 attaaaagag gggaatgtgt tttggccaaa ggaaccacaa tgggcccctc agagattggt     1320
266 cttctggcaa ctgtaggtgt cacagaggtt gaagttaata agtttcagt ggttgcatgc     1380

```

RAW SEQUENCE LISTING

DATE: 12/19/2006

PATENT APPLICATION: US/10/577,613A

TIME: 10:53:57

Input Set : A:\csequence listing.txt

Output Set: N:\CRF4\12192006\J577613A.raw

```

268 atgtcaacag ggaatgagct gctaaatcct gaagatgacc tcttaccagg gaagattcga 1440
270 gacagcaatc gttcaactct tctagcaaca attcaggaac atgggtaccc cacgatcaac 1500
272 ttgggtattg taggagacaa cccagatgac ttactcaatg ccttgaatga gggatatcagt 1560
274 cgtgctgatg tcatcatcac atcagggggg gtatccatgg gggaaaagga ctatctcaag 1620
276 caggtgctgg acattgatct tcatgctcag atccattttg gcagggtttt tatgaaacca 1680
278 ggcttgccaa caacatttgc aactttggat attgatgggt taagaaaaat aatctttgca 1740
280 ctacctggga atcctgtatc ggctgtgggc acctgcaatc tctttgttgt gcctgcactg 1800
282 aggaaaatgc agggcatctt ggatcctcgg ccaaccatca tcaaagcaag gttatcatgt 1860
284 gatgtaaaac ttgatcctcg tccagaatac catcgggtga tactaacttg gcatcaccaa 1920
286 gaaccactac cttgggcaca gagtacaggt aatcaaata gaagccgtct gatgagcatg 1980
288 cgcagtgcc aatggattgt gatgctacct ccaaagacag aacagtacgt ggagctccac 2040
290 aaaggcgagg tgggtgatgt catggtcatt ggacggctat gatggtcacc ag 2092

```

293 <210> SEQ ID NO: 3

294 <211> LENGTH: 300

295 <212> TYPE: PRT

296 <213> ORGANISM: Artificial

298 <220> FEATURE:

299 <223> OTHER INFORMATION: 2a SPA-5G-MBP

302 <220> FEATURE:

W--> 303 <221> NAME/KEY: FUSION_PRT

304 <222> LOCATION: (1)..(300)

305 <223> OTHER INFORMATION: Fusion Protein of Staph. aureus Protein A and H. sapiens MBP

307 <220> FEATURE:

308 <221> NAME/KEY: MISC_FEATURE

309 <222> LOCATION: (264)..(264)

310 <223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

312 <220> FEATURE:

313 <221> NAME/KEY: MISC_FEATURE

314 <222> LOCATION: (278)..(278)

315 <223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

317 <220> FEATURE:

318 <221> NAME/KEY: MISC_FEATURE

319 <222> LOCATION: (281)..(281)

320 <223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

322 <400> SEQUENCE: 3

```

324 Ala Ala Gln His Asp Glu Ala Gln Gln Asn Ala Phe Tyr Gln Val Leu
325 1          5          10          15
328 Asn Met Pro Asn Leu Asn Ala Asp Gln Arg Asn Gly Phe Ile Gln Ser
329          20          25          30
332 Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Val Leu Gly Glu Ala Lys
333          35          40          45
336 Lys Leu Asn Glu Ser Gln Ala Pro Lys Ala Asp Asn Asn Phe Asn Lys
337          50          55          60
340 Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu Asn Met Pro Asn Leu Asn
341 65          70          75          80
344 Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser
345          85          90          95
348 Gln Ser Ala Asn Leu Leu Ser Glu Ala Lys Lys Leu Asn Glu Ser Gln
349          100          105          110

```

RAW SEQUENCE LISTING

DATE: 12/19/2006

PATENT APPLICATION: US/10/577,613A

TIME: 10:53:57

Input Set : A:\csequence listing.txt

Output Set: N:\CRF4\12192006\J577613A.raw

```

352 Ala Pro Lys Ala Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe
353      115      120      125
356 Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Gly
357      130      135      140
360 Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu
361 145      150      155      160
364 Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Asp Asn
365      165      170      175
368 Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu
369      180      185      190
372 Pro Asn Leu Thr Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys
373      195      200      205
376 Asp Asp Pro Ser Val Ser Lys Glu Ile Leu Ala Glu Ala Lys Lys Leu
377      210      215      220
380 Asn Asp Ala Gln Ala Pro Lys Glu Glu Asp Asn Asn Lys Pro Gly Lys
381 225      230      235      240
384 Glu Asp Gly Asn Lys Pro Gly Lys Glu Asp Gly Asn Gly Gly Gly Gly
385      245      250      255
W--> 388 Gly Ala Ala Ala Ser Thr Ala Xaa Ala Ser Thr Ala Lys Glu Thr Ala
389      260      265      270
392 Glu Ala Val Ala Asp Xaa Ile Leu Xaa Lys Ala Gly Pro Leu Val Ala
393      275      280      285
396 Val Ser Ala Val Ala Leu Asp Ile Thr Ala Tyr Pro
397      290      295      300
400 <210> SEQ ID NO: 4
401 <211> LENGTH: 912
402 <212> TYPE: DNA
403 <213> ORGANISM: Artificial
405 <220> FEATURE:
406 <223> OTHER INFORMATION: 2b SPA-5g-MBP
409 <220> FEATURE:
410 <221> NAME/KEY: misc_recomb
411 <222> LOCATION: (1)..(912)
412 <223> OTHER INFORMATION: nucleic acid encoding Staph. aureus Protein A and H. sapiens
MBP
413      fusion prt
415 <220> FEATURE:
416 <221> NAME/KEY: misc_feature
417 <222> LOCATION: (792)..(792)
418 <223> OTHER INFORMATION: n is a, c, g, t or u
420 <220> FEATURE:
421 <221> NAME/KEY: misc_feature
422 <222> LOCATION: (835)..(835)
423 <223> OTHER INFORMATION: n is a, c, g, t or u
425 <220> FEATURE:
426 <221> NAME/KEY: misc_feature
427 <222> LOCATION: (844)..(844)
428 <223> OTHER INFORMATION: n is a, c, g, t or u
430 <400> SEQUENCE: 4
431 tgctgcgcaa cacgatgaag ctcaacaaaa cgctttttat caagtcttaa atatgcctaa      60

```

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/577,613A

DATE: 12/19/2006
TIME: 10:53:58

Input Set : A:\csequence listing.txt
Output Set: N:\CRF4\12192006\J577613A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; Xaa Pos. 264,278,281
Seq#:4; N Pos. 792,835,844
Seq#:8; N Pos. 488,531,540
Seq#:9; N Pos. 440,483,492
Seq#:12; N Pos. 792,835,844

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8,9,10,11,12,13,14

VERIFICATION SUMMARY

DATE: 12/19/2006

PATENT APPLICATION: US/10/577,613A

TIME: 10:53:58

Input Set : A:\csequence listing.txt

Output Set: N:\CRF4\12192006\J577613A.raw

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:28 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:303 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:388 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:256
M:341 Repeated in SeqNo=3
L:457 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:780
M:341 Repeated in SeqNo=4
L:856 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:480
L:932 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:420
M:341 Repeated in SeqNo=9
L:1314 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:780
M:341 Repeated in SeqNo=12